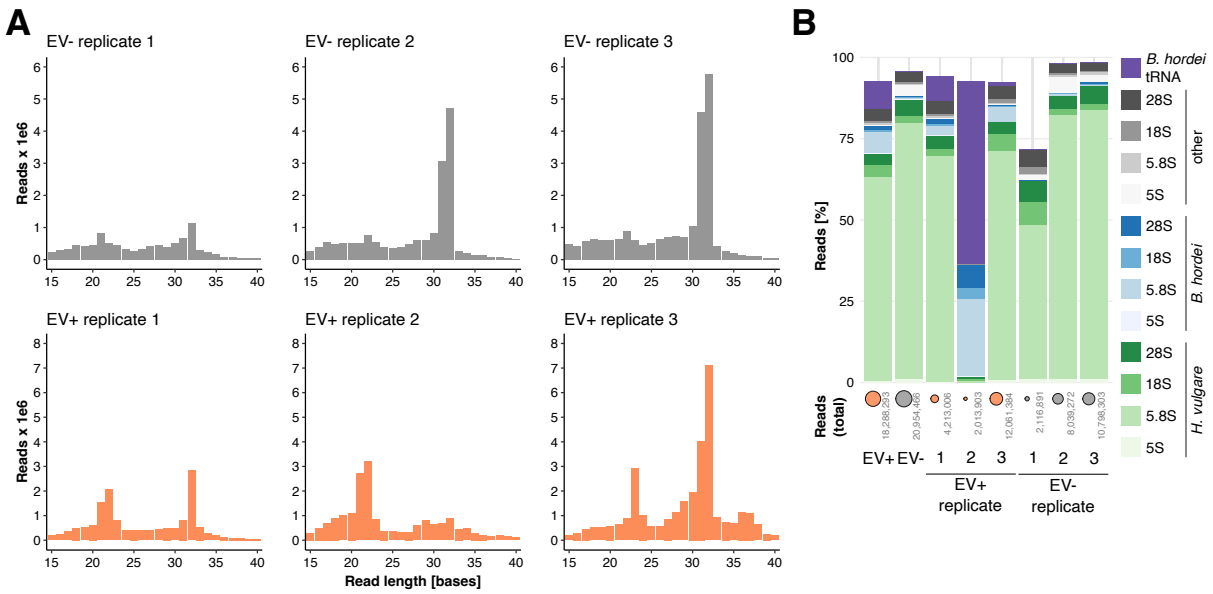

Supplementary Figure 10. EV- replicate three is more similar to EV samples from infected *H. vulgare* leaves. (**A**) Read length profiles for the three apoplastic extracellular vesicles of infected (EV+) and non-infected control plants (EV-) generated in this study. The histograms show the read counts (y-axis) for the respective read size (x-axis). (**B**) We aligned sRNA-seq reads of 31-32 bases in length to the RFAM database using MMSeqs2 (Steinegger and Söding 2017). The stacked bar graph shows the percentage of reads identified as 5S, 5.8S, 18S, 28S, or tRNA, as indicated in the color-coded legend. Green, reads identified as derived from *H. vulgare*; blue, reads identified as derived from *B. hordei* DH14; grey, reads originating from neither *H. vulgare* nor *B. hordei*; purple, reads identified as *B. hordei* tRNA-derived. Apoplastic extracellular vesicles (EV+), apoplastic extracellular vesicles of non-infected control plants (EV-), and the three EV+ and EV- replicates are shown. Total reads assigned to each sample are provided below the graph; circles visually indicate the total number of reads for comparison.